

#2

070  
1015

OIPE

## RAW SEQUENCE LISTING

DATE: 01/26/2002

PATENT APPLICATION: US/09/809,617

TIME: 13:46:01

Input Set : N:\Cr3\RULE60\09809617.raw

Output Set: N:\CRF3\01252002\I809617.raw

1 <110> APPLICANT: Sheppard, Paul O.  
2 Baindur, Nand  
3 Deisher, Theresa A.  
4 Bishop, Paul D.  
5 <120> TITLE OF INVENTION: DISINTEGRIN HOMOLOG  
6 <130> FILE REFERENCE: 98-29  
7 <140> CURRENT APPLICATION NUMBER: 09/809,617  
8 <141> CURRENT FILING DATE: 2001-03-15  
10 <150> PRIOR APPLICATION NUMBER: US/09/351,414  
11 <151> PRIOR FILING DATE: 1999-07-09  
14 <160> NUMBER OF SEQ ID NOS: 13  
15 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 2268  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Homo sapiens  
21 <220> FEATURE:  
22 <221> NAME/KEY: CDS  
23 <222> LOCATION: (3)...(2090)  
24 <221> NAME/KEY: misc\_feature  
25 <222> LOCATION: (1)...(2268)  
26 <223> OTHER INFORMATION: n = A,T,C or G  
27 <400> SEQUENCE: 1  
28 cc act gtg ttg gaa ttc ggc acg agg ctt gac aca aag gca aga cac 47  
29 Thr Val Leu Glu Phe Gly Thr Arg Leu Asp Thr Lys Ala Arg His  
30 1 5 10 15  
31 cag caa aaa cat aat aag gct gtc cat ctg gcc cag gca agc ttc cag 95  
32 Gln Gln Lys His Asn Lys Ala Val His Leu Ala Gln Ala Ser Phe Gln  
33 20 25 30  
34 att gaa gcc ttc ggc tcc aaa ttc att ctt gac ctc ata ctg aac aat 143  
35 Ile Glu Ala Phe Gly Ser Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn  
36 35 40 45  
37 ggt ttg ttg tct tct gat tat gtg gag att cac tac gaa aat ggg aaa 191  
38 Gly Leu Leu Ser Ser Asp Tyr Val Glu Ile His Tyr Glu Asn Gly Lys  
39 50 55 60  
40 cca cag tac tct aag ggt gga gag cac tgt tac tac cat gga agc atc 239  
41 Pro Gln Tyr Ser Lys Gly Gly Glu His Cys Tyr Tyr His Gly Ser Ile  
42 65 70 75  
43 aga ggc gtc aaa gac tcc aag gtg gct ctg tca acc tgc aat gga ctt 287  
44 Arg Gly Val Lys Asp Ser Lys Val Ala Leu Ser Thr Cys Asn Gly Leu  
45 80 85 90 95  
46 cat ggc atg ttt gaa gat gat acc ttc gtg tat atg ata gag cca cta 335  
47 His Gly Met Phe Glu Asp Asp Thr Phe Val Tyr Met Ile Glu Pro Leu

ENTERED

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48					100					105				110				
49	gag	ctg	gtt	cat	gat	gag	aaa	agc	aca	ggt	cga	cca	cat	ata	atc	cag		383
50	Glu	Leu	Val	His	Asp	Glu	Lys	Ser	Thr	Gly	Arg	Pro	His	Ile	Ile	Gln		
51					115					120				125				
52	aaa	acc	ttg	gca	gga	cag	tat	tct	aag	caa	atg	aag	aat	ctc	act	atg		431
53	Lys	Thr	Leu	Ala	Gly	Gln	Tyr	Ser	Lys	Gln	Met	Lys	Asn	Leu	Thr	Met		
54					130					135				140				
55	gaa	aga	ggt	gac	cag	tgg	ccc	ttt	ctc	tct	gaa	tta	cag	tgg	ttg	aaa		479
56	Glu	Arg	Gly	Asp	Gln	Trp	Pro	Phe	Leu	Ser	Glu	Leu	Gln	Trp	Leu	Lys		
57					145					150				155				
58	aga	agg	aag	aga	gca	gtg	aat	cca	tca	cgt	ggt	ata	ttt	gaa	gaa	atg		527
59	Arg	Arg	Lys	Arg	Ala	Val	Asn	Pro	Ser	Arg	Gly	Ile	Phe	Glu	Glu	Met		
60					160						170					175		
61	aaa	tat	ttg	gaa	ctt	atg	att	ggt	aat	gat	cac	aaa	acg	tat	aag	aag		575
62	Lys	Tyr	Leu	Glu	Leu	Met	Ile	Gly	Asn	Asp	His	Lys	Thr	Tyr	Lys	Lys		
63					180						185				190			
64	cat	cgc	tct	tct	cat	gca	cat	acc	aac	aac	ttt	gca	aag	tcc	gtg	gtc		623
65	His	Arg	Ser	Ser	His	Ala	His	Thr	Asn	Asn	Phe	Ala	Lys	Ser	Val	Val		
66					195					200				205				
67	aac	ctt	gtg	gat	tct	att	tac	aag	gag	cag	ctc	aac	acc	agg	gtt	gtc		671
68	Asn	Leu	Val	Asp	Ser	Ile	Tyr	Lys	Glu	Gln	Leu	Asn	Thr	Arg	Val	Val		
69					210					215				220				
70	ctg	gtg	gct	gta	gag	acc	tgg	act	gag	aag	gat	cag	att	gac	atc	acc		719
71	Leu	Val	Ala	Val	Glu	Thr	Trp	Thr	Glu	Lys	Asp	Gln	Ile	Asp	Ile	Thr		
72					225						230			235				
73	acc	aac	cct	gtg	cag	atg	ctc	cat	gag	ttc	tca	aaa	tac	cgg	cag	cgc		767
74	Thr	Asn	Pro	Val	Gln	Met	Leu	His	Glu	Phe	Ser	Lys	Tyr	Arg	Gln	Arg		
75					240					245				250		255		
76	att	aag	cag	cat	gct	gat	gct	gtg	cac	ctc	atc	tcg	cgg	gtg	aca	ttt		815
77	Ile	Lys	Gln	His	Ala	Asp	Ala	Val	His	Leu	Ile	Ser	Arg	Val	Thr	Phe		
78					260					265				270				
79	cac	tat	aag	aga	agc	agt	ctg	agt	tac	ttt	gaa	ggt	gtc	tgt	tct	cgc		863
80	His	Tyr	Lys	Arg	Ser	Ser	Leu	Ser	Tyr	Phe	Glu	Gly	Val	Cys	Ser	Arg		
81					275					280				285				
82	aca	aga	gga	gtt	ggt	gtg	aat	gag	tat	ggt	ctt	cca	atg	gca	gtg	gca		911
83	Thr	Arg	Gly	Val	Gly	Val	Asn	Glu	Tyr	Gly	Leu	Pro	Met	Ala	Val	Ala		
84					290					295				300				
85	caa	gta	tta	tcg	cag	agc	ctg	gct	caa	aac	ctt	gga	atc	caa	tgg	gaa		959
86	Gln	Val	Leu	Ser	Gln	Ser	Leu	Ala	Gln	Asn	Leu	Gly	Ile	Gln	Trp	Glu		
87					305					310				315				
88	cct	tct	agc	aga	aag	cca	aaa	tgt	gac	tgc	aca	gaa	tcc	tgg	ggt	ggc		1007
89	Pro	Ser	Ser	Arg	Lys	Pro	Lys	Cys	Asp	Cys	Thr	Glu	Ser	Trp	Gly	Gly		
90					320					325				330		335		
91	tgc	atc	atg	gag	gaa	aca	ggg	gtg	tcc	cat	tct	cga	aaa	ttt	tca	aag		1055
92	Cys	Ile	Met	Glu	Glu	Thr	Gly	Val	Ser	His	Ser	Arg	Lys	Phe	Ser	Lys		
93					340					345				350				
94	tgc	agc	att	ttg	gag	tat	aga	gac	ttt	tta	cag	aga	gga	ggt	gga	gcc		1103
95	Cys	Ser	Ile	Leu	Glu	Tyr	Arg	Asp	Phe	Leu	Gln	Arg	Gly	Gly	Gly	Ala		
96					355					360				365				

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97	tgc ctt ttc aac agg cca aca aag cta ttt gag ccc acg gaa tgt gga	1151
98	Cys Leu Phe Asn Arg Pro Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly	
99	370 375 380	
100	aat gga tac gtg gaa gct ggg gag gag tgt gat tgt ggt ttt cat gtg	1199
101	Asn Gly Tyr Val Glu Ala Gly Glu Glu Cys Asp Cys Gly Phe His Val	
102	385 390 395	
103	gaa tgc tat gga tta tgc tgt aag aaa tgt tcc ctc tcc aac ggg gct	1247
104	Glu Cys Tyr Gly Leu Cys Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala	
105	400 405 410 415	
106	cac tgc agc gac ggg ccc tgc tgt aac aat acc tca tgt ctt ttt cag	1295
107	His Cys Ser Asp Gly Pro Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln	
108	420 425 430	
109	cca cga ggg tat gaa tgc cgg gat gct gtg aac gag tgt gat att act	1343
110	Pro Arg Gly Tyr Glu Cys Arg Asp Ala Val Asn Glu Cys Asp Ile Thr	
111	435 440 445	
112	gaa tat tgt act gga gac tct ggt cag tgc cca cca aat ctt cat aag	1391
113	Glu Tyr Cys Thr Gly Asp Ser Gly Gln Cys Pro Pro Asn Leu His Lys	
114	450 455 460	
115	caa gac gga tat gca tgc aat caa aat cag ggc cgc tgc tac aat ggc	1439
116	Gln Asp Gly Tyr Ala Cys Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly	
117	465 470 475	
118	gag tgc aag acc aga gac aac cag tgt cag tac atc tgg gga aca aag	1487
119	Glu Cys Lys Thr Arg Asp Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys	
120	480 485 490 495	
121	gct gca ggg tct gac aag ttc tgc tat gaa aag ctg aat aca gaa ggc	1535
122	Ala Ala Gly Ser Asp Lys Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly	
123	500 505 510	
124	act gag aag gga aac tgc ggg aag gat gga gac cgg tgg att cag tgc	1583
125	Thr Glu Lys Gly Asn Cys Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys	
126	515 520 525	
127	agc aaa cat gat gtg ttc tgt gga ttc tta ctc tgt acc aat ctt act	1631
128	Ser Lys His Asp Val Phe Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr	
129	530 535 540	
130	cga gct cca cgt att ggt caa ctt cag ggt gag atc att cca act tcc	1679
131	Arg Ala Pro Arg Ile Gly Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser	
132	545 550 555	
133	ttc tac cat caa ggc cgg gtg att gac tgc agt ggt gcc cat gta gtt	1727
134	Phe Tyr His Gln Gly Arg Val Ile Asp Cys Ser Gly Ala His Val Val	
135	560 565 570 575	
136	tta gat gat gat acg gat gtg ggc tat gta gaa gat gga acg cca tgt	1775
137	Leu Asp Asp Asp Thr Asp Val Gly Tyr Val Glu Asp Gly Thr Pro Cys	
138	580 585 590	
139	ggc ccg tct atg atg tgt tta gat cgg aag tgc cta caa att caa gcc	1823
140	Gly Pro Ser Met Met Cys Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala	
141	595 600 605	
142	cta aat atg agc agc tgt cca ctc gat tcc aag ggt aaa gtc tgt tcg	1871
143	Leu Asn Met Ser Ser Cys Pro Leu Asp Ser Lys Gly Lys Val Cys Ser	
144	610 615 620	
145	ggc cat ggg gtg tgt agt aat gaa gcc acc tgc att tgt gat ttc acc	1919

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146      Gly His Gly Val Cys Ser Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr
147          625                      630                      635
148      tgg gca ggg aca gat tgc agt atc cgg gat cca gtt agg aac ctt cac      1967
149      Trp Ala Gly Thr Asp Cys Ser Ile Arg Asp Pro Val Arg Asn Leu His
150          640                      645                      650                      655
151      ccc ccc aag gat gaa gga ccc aag ggt ttg tgt gat ttt ggt ttc aat      2015
152      Pro Pro Lys Asp Glu Gly Pro Lys Gly Leu Cys Asp Phe Gly Phe Asn
153          660                      665                      670
154      tca tgg aat act gaa ttc gtt gac act gtt cca atg cac cag tat aac      2063
155      Ser Trp Asn Thr Glu Phe Val Asp Thr Val Pro Met His Gln Tyr Asn
156          675                      680                      685
W--> 157      att cta att gac tta aga gga gac aca taagaatatc ngtttttgcc      2110
158      Ile Leu Ile Asp Leu Arg Gly Asp Thr
159          690                      695
160      ttttaaagtat ataatttatg ttactgccaa attaaggatt ctgatatatc atatttttaa      2170
161      aatgtgtttg aattacttct tagtctagaa ctgagattgg gaagaagtaa atatacacat      2230
162      tttctttaat acagtattct ttttctcttt aaacctta      2268
164 <210> SEQ ID NO: 2
165 <211> LENGTH: 696
166 <212> TYPE: PRT
167 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 2
169      Thr Val Leu Glu Phe Gly Thr Arg Leu Asp Thr Lys Ala Arg His Gln
170          1                      5                      10                      15
171      Gln Lys His Asn Lys Ala Val His Leu Ala Gln Ala Ser Phe Gln Ile
172          20                      25                      30
173      Glu Ala Phe Gly Ser Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn Gly
174          35                      40                      45
175      Leu Leu Ser Ser Asp Tyr Val Glu Ile His Tyr Glu Asn Gly Lys Pro
176          50                      55                      60
177      Gln Tyr Ser Lys Gly Gly Glu His Cys Tyr Tyr His Gly Ser Ile Arg
178          65                      70                      75                      80
179      Gly Val Lys Asp Ser Lys Val Ala Leu Ser Thr Cys Asn Gly Leu His
180          85                      90                      95
181      Gly Met Phe Glu Asp Asp Thr Phe Val Tyr Met Ile Glu Pro Leu Glu
182          100                      105                      110
183      Leu Val His Asp Glu Lys Ser Thr Gly Arg Pro His Ile Gln Lys
184          115                      120                      125
185      Thr Leu Ala Gly Gln Tyr Ser Lys Gln Met Lys Asn Leu Thr Met Glu
186          130                      135                      140
187      Arg Gly Asp Gln Trp Pro Phe Leu Ser Glu Leu Gln Trp Leu Lys Arg
188          145                      150                      155                      160
189      Arg Lys Arg Ala Val Asn Pro Ser Arg Gly Ile Phe Glu Glu Met Lys
190          165                      170                      175
191      Tyr Leu Glu Leu Met Ile Gly Asn Asp His Lys Thr Tyr Lys Lys His
192          180                      185                      190
193      Arg Ser Ser His Ala His Thr Asn Asn Phe Ala Lys Ser Val Val Asn
194          195                      200                      205
195      Leu Val Asp Ser Ile Tyr Lys Glu Gln Leu Asn Thr Arg Val Val Leu

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196	210	215	220
197	Val Ala Val Glu Thr Trp Thr Glu Lys Asp Gln Ile Asp Ile Thr Thr		
198	225	230	235
199	Asn Pro Val Gln Met Leu His Glu Phe Ser Lys Tyr Arg Gln Arg Ile		240
200		245	250
201	Lys Gln His Ala Asp Ala Val His Leu Ile Ser Arg Val Thr Phe His		255
202		260	265
203	Tyr Lys Arg Ser Ser Leu Ser Tyr Phe Glu Gly Val Cys Ser Arg Thr		270
204		275	280
205	Arg Gly Val Gly Val Asn Glu Tyr Gly Leu Pro Met Ala Val Ala Gln		285
206		290	295
207	Val Leu Ser Gln Ser Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu Pro		300
208	305	310	315
209	Ser Ser Arg Lys Pro Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly Cys		320
210		325	330
211	Ile Met Glu Glu Thr Gly Val Ser His Ser Arg Lys Phe Ser Lys Cys		335
212		340	345
213	Ser Ile Leu Glu Tyr Arg Asp Phe Leu Gln Arg Gly Gly Gly Ala Cys		350
214		355	360
215	Leu Phe Asn Arg Pro Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly Asn		365
216		370	375
217	Gly Tyr Val Glu Ala Gly Glu Glu Cys Asp Cys Gly Phe His Val Glu		380
218	385	390	395
219	Cys Tyr Gly Leu Cys Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala His		400
220		405	410
221	Cys Ser Asp Gly Pro Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln Pro		415
222		420	425
223	Arg Gly Tyr Glu Cys Arg Asp Ala Val Asn Glu Cys Asp Ile Thr Glu		430
224		435	440
225	Tyr Cys Thr Gly Asp Ser Gly Gln Cys Pro Pro Asn Leu His Lys Gln		445
226		450	455
227	Asp Gly Tyr Ala Cys Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly Glu		460
228	465	470	475
229	Cys Lys Thr Arg Asp Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys Ala		480
230		485	490
231	Ala Gly Ser Asp Lys Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly Thr		495
232		500	505
233	Glu Lys Gly Asn Cys Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys Ser		510
234		515	520
235	Lys His Asp Val Phe Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr Arg		525
236		530	535
237	Ala Pro Arg Ile Gly Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser Phe		540
238	545	550	555
239	Tyr His Gln Gly Arg Val Ile Asp Cys Ser Gly Ala His Val Val Leu		560
240		565	570
241	Asp Asp Asp Thr Asp Val Gly Tyr Val Glu Asp Gly Thr Pro Cys Gly		575
242		580	585
243	Pro Ser Met Cys Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala Leu		590
244		595	600
			605

## VERIFICATION SUMMARY

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TIME: 13:46:02

Input Set : N:\Crf3\RULE60\09809617.raw

Output Set: N:\CRF3\01252002\I809617.raw

L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
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L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3